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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=14; hr=10; min=53; sec=45; ms=828; ]

=====

\*\*\*\*\*

Reviewer Comments:

<210> 1

<211> 654

<212> DNA

<213> Escherichia coli K12

Please adjust the above <213> response to "Escherichia coli" only, and move the explanatory information to the <220>-<223> section. Per 1.823 of the Sequence Rules, the only valid <213> responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown."

"Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section: please give the source of the genetic material. The above type of response appears in subsequent sequences, too: please adjust them.

<210> 4

<211> 256

<212> PRT

<213> Escherichia coli K12 nfnB in pET-28(a)(+); pMKS2

<220>

<221> misc\_feature

<222> (250)..(267)

<223> Cys tags

<220>

<221> misc\_feature

<222> (160)..(177)

<223> His tags

<220>

<221> misc\_feature

<222> (268)..(285)

<223> primer

<220>

<221> misc\_feature

<222> (996)..(1010)

<223> primer

<400> 4

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5					10					15	

Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg
			20					25					30		

Gly	Ser	Cys	Cys	Cys	Cys	Cys	Cys	Asp	Ile	Ile	Ser	Val	Ala	Leu	Lys
		35					40					45			

Arg His Ser Thr Lys Ala Phe Asp Ala Ser Lys Lys Leu Thr Pro Glu  
50 55 60

Gln Ala Glu Gln Ile Lys Thr Leu Leu Gln Tyr Ser Pro Ser Ser Thr  
65 70 75 80

Asn Ser Gln Pro Trp His Phe Ile Val Ala Ser Thr Glu Glu Gly Lys  
85 90 95

Ala Arg Val Ala Lys Ser Ala Ala Gly Asn Tyr Val Phe Asn Glu Arg  
100 105 110

Lys Met Leu Asp Ala Ser His Val Val Val Phe Cys Ala Lys Thr Ala  
115 120 125

Met Asp Asp Val Trp Leu Lys Leu Val Val Asp Gln Glu Asp Ala Asp  
130 135 140

Gly Arg Phe Ala Thr Pro Glu Ala Lys Ala Ala Asn Asp Lys Gly Arg  
145 150 155 160

Lys Phe Phe Ala Asp Met His Arg Lys Asp Leu His Asp Asp Ala Glu  
165 170 175

Trp Met Ala Lys Gln Val Tyr Leu Asn Val Gly Asn Phe Leu Leu Gly  
180 185 190

Val Ala Ala Leu Gly Leu Asp Ala Val Pro Ile Glu Gly Phe Asp Ala  
195 200 205

Ala Ile Leu Asp Ala Glu Phe Gly Leu Lys Glu Lys Gly Tyr Thr Ser  
210 215 220

Leu Val Val Val Pro Val Gly His His Ser Val Glu Asp Phe Asn Ala  
225 230 235 240

Thr Leu Pro Lys Ser Arg Leu Pro Gln Asn Ile Thr Leu Thr Glu Val  
245 250 255

Please remove the <220>-<223> sections (as shown below) because Sequence 4 only has 256 amino acids:

<220>

<221> misc\_feature

<222> (250)..(267)

<223> Cys tags

<220>

<221> misc\_feature

<222> (268)..(285)

<223> primer

<220>

<221> misc\_feature

<222> (996)..(1010)

<223> primer

Same type of error in Sequence 6.

(end of Sequence 9)

<400> 9

ggatcctggtt gctggttgctg ttgcatatc atttctgtcg cc

42

1/11

Please remove the above "1/11" which appears at the end of the submitted file.

\*\*\*\*\*

Application No: 10582557 Version No: 1.0

Input Set:

Output Set:

Started: 2008-08-14 09:58:35.104  
Finished: 2008-08-14 09:58:36.041  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 937 ms  
Total Warnings: 7  
Total Errors: 1  
No. of SeqIDs Defined: 9  
Actual SeqID Count: 9

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)

# SEQUENCE LISTING

<110> University of Wales, Bangor

Trwyn Ltd

<120> Improvements In and Relating to Biosensors

<130> BA/SLH/Y1861

<140> 10582557

<141> 2008-08-14

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 654

<212> DNA

<213> Escherichia coli K12

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accaactccc agccgtggca ttttattggt gccagcacgg aagaaggtaa agcgcgtggt	180
gccaaatccg ctgccggtaa ttacgtgttc aacgagcgta aaatgcttga tgctcgcac	240
gtcgtggtgt tctgtgcaaa aaccgcatg gacgatgtct ggctgaagct ggttggtgac	300
caggaagatg ccgatggccg ctttgccacg ccggaagcga aagccgcgaa cgataaaggt	360
cgcaagttct tcgctgatat gcaccgtaaa gatctgcatg atgatgcaga gtggatggca	420
aaacaggttt atctcaacgt cggtaacttc ctgctcggcg tggcggctct gggctctggac	480
gcggtacca tcgaaggttt tgacgccgcc atcctcgatg cagaatttgg tctgaaagag	540
aaaggctaca ccagtctggt ggttggtccg gtaggtcatc acagcgttga agattttaac	600
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<210> 2

<211> 826

<212> DNA

<213> *Pseudomonas putida* JLR11

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agcgatcttc ctgtggatga gcagatgctg agctgggcga tcgcggcggc ccagtcagcc	180
tcgacttcct cgaacctgca agcttggagc gtgctcgccg tgcgggatcg cgagcgtctc	240
gcgaggcttg cccgactgtc cggtaaccag cgccatgtcg agcaggcacc gctgttcctg	300
gtctggctcg tggactggtc acgcctacgc cgactagcca gaacccttca ggcaccgact	360
gcaggtatcg actatthaga aagctacacc gtcggtgttg tagatgcagc tctggccgct	420
cagaacgccg cactagcttt cgaggcccaa ggactgggaa tcgtttacat cggcggaatg	480
cgcaaccacc cggaagcgat gtccgaggag cttggcctgc caaacgacac tttcgctgta	540
tttggcatgt gcgtcgggtca tcccgatccg gcacagcccc ccgagatcaa gccacgcctg	600
gcgcaatcag tgggtgcttca ccgtgagcgc tatgaggcca ccgaggcaga ggcggtttca	660
gttgetgcct atgaccgaag gatgagcgac ttccaacatc gtcaacaacg cgaaaaccgt	720
tcctgggtcca gccaggccgt ggaacgtgta aaaggagcgg attcactgag cggaagacac	780
cgcttgcgag atgcattaaa caccctaggt ttcggcctgc gctgag	826

<210> 3

<211> 1066

<212> DNA

<213> *Escherichia coli* K12 nfnB in pET-28(a)(+); pMKS2

<220>

<221> CDS

<222> (88)..(858)

<223> Coding sequence for nfnB gene



<220>

<221> misc\_feature

<222> (250)..(267)

<223> Cys tags

<220>

<221> misc\_feature

<222> (160)..(177)

<223> His tags

<220>

<221> misc\_feature

<222> (268)..(285)

<223> primer

<220>

<221> misc\_feature

<222> (996)..(1010)

<223> primer

<400> 3

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tggtttaactt taagaaggag atatacc atg ggc agc agc cat cat cat cat cat 114

Met Gly Ser Ser His His His His His

1 5

cac agc agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act 162

His Ser Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr

10 15 20 25

ggt gga cag caa atg ggt cgc gga tcc tgt tgc tgt tgc tgt tgc gat 210

Gly Gly Gln Gln Met Gly Arg Gly Ser Cys Cys Cys Cys Cys Cys Asp

30 35 40

atc att tct gtc gcc tta aag cgt cat tcc act aag gca ttt gat gcc	258
Ile Ile Ser Val Ala Leu Lys Arg His Ser Thr Lys Ala Phe Asp Ala	
45 50 55	
agc aaa aaa ctt acc ccg gaa cag gcc gag cag atc aaa acg cta ctg	306
Ser Lys Lys Leu Thr Pro Glu Gln Ala Glu Gln Ile Lys Thr Leu Leu	
60 65 70	
caa tac agc cca tcc agc acc aac tcc cag ccg tgg cat ttt att gtt	354
Gln Tyr Ser Pro Ser Ser Thr Asn Ser Gln Pro Trp His Phe Ile Val	
75 80 85	
gcc agc acg gaa gaa ggt aaa gcg cgt gtt gcc aaa tcc gct gcc ggt	402
Ala Ser Thr Glu Glu Gly Lys Ala Arg Val Ala Lys Ser Ala Ala Gly	
90 95 100 105	
aat tac gtg ttc aac gag cgt aaa atg ctt gat gcc tcg cac gtc gtg	450
Asn Tyr Val Phe Asn Glu Arg Lys Met Leu Asp Ala Ser His Val Val	
110 115 120	
gtg ttc tgt gca aaa acc gcg atg gac gat gtc tgg ctg aag ctg gtt	498
Val Phe Cys Ala Lys Thr Ala Met Asp Asp Val Trp Leu Lys Leu Val	
125 130 135	
gtt gac cag gaa gat gcc gat ggc cgc ttt gcc acg ccg gaa gcg aaa	546
Val Asp Gln Glu Asp Ala Asp Gly Arg Phe Ala Thr Pro Glu Ala Lys	
140 145 150	
gcc gcg aac gat aaa ggt cgc aag ttc ttc gct gat atg cac cgt aaa	594
Ala Ala Asn Asp Lys Gly Arg Lys Phe Phe Ala Asp Met His Arg Lys	
155 160 165	
gat ctg cat gat gat gca gag tgg atg gca aaa cag gtt tat ctc aac	642
Asp Leu His Asp Asp Ala Glu Trp Met Ala Lys Gln Val Tyr Leu Asn	
170 175 180 185	
gtc ggt aac ttc ctg ctc ggc gtg gcg gct ctg ggt ctg gac gcg gta	690
Val Gly Asn Phe Leu Leu Gly Val Ala Ala Leu Gly Leu Asp Ala Val	
190 195 200	
ccc atc gaa ggt ttt gac gcc gcc atc ctc gat gca gaa ttt ggt ctg	738
Pro Ile Glu Gly Phe Asp Ala Ala Ile Leu Asp Ala Glu Phe Gly Leu	
205 210 215	
aaa gag aaa ggc tac acc agt ctg gtg gtt gtt ccg gta ggt cat cac	786
Lys Glu Lys Gly Tyr Thr Ser Leu Val Val Val Pro Val Gly His His	
220 225 230	
agc gtt gaa gat ttt aac gct acg ctg ccg aaa tct cgt ctg ccg caa	834
Ser Val Glu Asp Phe Asn Ala Thr Leu Pro Lys Ser Arg Leu Pro Gln	
235 240 245	
aac atc acc tta acc gaa gtg taa ttctctcttg ccgggcatct gcccggtat	888
Asn Ile Thr Leu Thr Glu Val	
250 255	
ttctctcag attctcctga ttgcataac cctgtttcag caagcttcgt catcataggc	948

tgctgttgaa gcttgcggcc gcactcgagc accaccacca ccaccactga gatccggctg 1008

ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa taactagc 1066

<210> 4

<211> 256

<212> PRT

<213> Escherichia coli K12 nfnB in pET-28(a)(+); pMKS2

<220>

<221> misc\_feature

<222> (250)..(267)

<223> Cys tags

<220>

<221> misc\_feature

<222> (160)..(177)

<223> His tags

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<222> (268)..(285)

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<221> misc\_feature

<222> (996)..(1010)

<223> primer

<400> 4

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5					10					15	
Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg
			20					25					30		

Gly	Ser	Cys	Cys	Cys	Cys	Cys	Cys	Asp	Ile	Ile	Ser	Val	Ala	Leu	Lys
		35					40					45			
Arg	His	Ser	Thr	Lys	Ala	Phe	Asp	Ala	Ser	Lys	Lys	Leu	Thr	Pro	Glu
	50					55					60				
Gln	Ala	Glu	Gln	Ile	Lys	Thr	Leu	Leu	Gln	Tyr	Ser	Pro	Ser	Ser	Thr
65					70					75					80
Asn	Ser	Gln	Pro	Trp	His	Phe	Ile	Val	Ala	Ser	Thr	Glu	Glu	Gly	Lys
				85					90					95	
Ala	Arg	Val	Ala	Lys	Ser	Ala	Ala	Gly	Asn	Tyr	Val	Phe	Asn	Glu	Arg
			100					105					110		
Lys	Met	Leu	Asp	Ala	Ser	His	Val	Val	Val	Phe	Cys	Ala	Lys	Thr	Ala
		115					120					125			
Met	Asp	Asp	Val	Trp	Leu	Lys	Leu	Val	Val	Asp	Gln	Glu	Asp	Ala	Asp
	130					135					140				
Gly	Arg	Phe	Ala	Thr	Pro	Glu	Ala	Lys	Ala	Ala	Asn	Asp	Lys	Gly	Arg
145					150					155					160
Lys	Phe	Phe	Ala	Asp	Met	His	Arg	Lys	Asp	Leu	His	Asp	Asp	Ala	Glu
			165						170					175	
Trp	Met	Ala	Lys	Gln	Val	Tyr	Leu	Asn	Val	Gly	Asn	Phe	Leu	Leu	Gly
		180						185					190		
Val	Ala	Ala	Leu	Gly	Leu	Asp	Ala	Val	Pro	Ile	Glu	Gly	Phe	Asp	Ala
		195					200					205			
Ala	Ile	Leu	Asp	Ala	Glu	Phe	Gly	Leu	Lys	Glu	Lys	Gly	Tyr	Thr	Ser
	210					215					220				
Leu	Val	Val	Val	Pro	Val	Gly	His	His	Ser	Val	Glu	Asp	Phe	Asn	Ala
225					230					235					240
Thr	Leu	Pro	Lys	Ser	Arg	Leu	Pro	Gln	Asn	Ile	Thr	Leu	Thr	Glu	Val
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<210> 5

<211> 1221

<212> DNA

<213> Pseudomonas putida JLR11 prnB in pET-28(a) (+) ; pKMS6

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<222> (88) .. (1029)

<223>

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<222> (190) .. (225)

<223> primer

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<222> (190) .. (207)

<223> cys tag

<220>

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<222> (936) .. (956)

<223> primer

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tggtttaactt taagaaggag atatacc atg ggc agc agc cat cat cat cat cat 114

Met Gly Ser Ser His His His His His

1 5

cac agc agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act	162
His Ser Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr	
10 15 20 25	
ggt gga cag caa atg ggt cgc gga tcc tgt tgc tgt tgc tgt tgc agc	210
Gly Gly Gln Gln Met Gly Arg Gly Ser Cys Cys Cys Cys Cys Cys Ser	
30 35 40	
ctt caa gac gaa gca ctc aaa gcc tgg caa gcc cgt tat ggc gag cca	258
Leu Gln Asp Glu Ala Leu Lys Ala Trp Gln Ala Arg Tyr Gly Glu Pro	
45 50 55	
gct aac tta cct gct gcc gac acc gtg atc gcg cag atg ttg cag cat	306
Ala Asn Leu Pro Ala Ala Asp Thr Val Ile Ala Gln Met Leu Gln His	
60 65 70	
cga tca gta cgt gcc tac agc gat ctt cct gtg gat gag cag atg ctg	354
Arg Ser Val Arg Ala Tyr Ser Asp Leu Pro Val Asp Glu Gln Met Leu	
75 80 85	
agc tgg gcg atc gcg gcg gcc cag tca gcc tcg act tcc tcg aac ctg	402
Ser Trp Ala Ile Ala Ala Ala Gln Ser Ala Ser Thr Ser Ser Asn Leu	
90 95 100 105	
caa gct tgg agc gtg ctc gcc gtg cgg gat cgc gag cgt ctc gcg agg	450
Gln Ala Trp Ser Val Leu Ala Val Arg Asp Arg Glu Arg Leu Ala Arg	
110 115 120	
ctt gcc cga ctg tcc ggt aac cag cgc cat gtc gag cag gca ccg ctg	498
Leu Ala Arg Leu Ser Gly Asn Gln Arg His Val Glu Gln Ala Pro Leu	
125 130 135	
ttc ctg gtc tgg ctc gtg gac tgg tca cgc cta cgc cga cta gcc aga	546
Phe Leu Val Trp Leu Val Asp Trp Ser Arg Leu Arg Arg Leu Ala Arg	
140 145 150	
acc ctt cag gca ccg act gca ggt atc gac tat tta gaa agc tac acc	594
Thr Leu Gln Ala Pro Thr Ala Gly Ile Asp Tyr Leu Glu Ser Tyr Thr	
155 160 165	
gtc ggt gtt gta gat gca gct ctg gcc gct cag aac gcc gca cta gct	642
Val Gly Val Val Asp Ala Ala Leu Ala Ala Gln Asn Ala Ala Leu Ala	
170 175 180 185	
ttc gag gcc caa gga ctg gga atc gtt tac atc ggc gga atg cgc aac	690
Phe Glu Ala Gln Gly Leu Gly Ile Val Tyr Ile Gly Gly Met Arg Asn	
190 195 200	
cac ccg gaa gcg atg tcc gag gag ctt ggc ctg cca aac gac act ttc	738
His Pro Glu Ala Met Ser Glu Glu Leu Gly Leu Pro Asn Asp Thr Phe	
205 210 215	
gct gta ttt ggc atg tgc gtc ggt cat ccc gat ccg gca cag ccc gcc	786
Ala Val Phe Gly Met Cys Val Gly His Pro Asp Pro Ala Gln Pro Ala	
220 225 230	

gag atc aag cca cgc ctg gcg caa tca gtg gtg ctt cac cgt gag cgc	834
Glu Ile Lys Pro Arg Leu Ala Gln Ser Val Val Leu His Arg Glu Arg	
235 240 245	
tat gag gcc acc gag gca gag gcg gtt tca gtt gct gcc tat gac cga	882
Tyr Glu Ala Thr Glu Ala Glu Ala Val Ser Val Ala Ala Tyr Asp Arg	
250 255 260 265	
agg atg agc gac ttc caa cat cgt caa caa cgc gaa aac cgt tcc tgg	930
Arg Met Ser Asp Phe Gln His Arg Gln Gln Arg Glu Asn Arg Ser Trp	
270 275 280	
tcc agc cag gcc gtg gaa cgt gta aaa gga gcg gat tca ctg agc gga	978
Ser Ser Gln Ala Val Glu Arg Val Lys Gly Ala Asp Ser Leu Ser Gly	
285 290 295	
aga cac cgc ttg cga gat gca tta aac acc cta ggt ttc ggc ctg cgc	1026
Arg His Arg Leu Arg Asp Ala Leu Asn Thr Leu Gly Phe Gly Leu Arg	
300 305 310	
tga gatagtgaga tatcccatgc ctattcccgc cgccctgaac cggagcacta	1079
atacctggca actttgcttg agctccgtcg acaagcttgc ggccgcactc gagcaccacc	1139
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<210> 6

<211> 313

<212> PRT

<213> Pseudomonas putida JLR11 prnB in pET-28(a)(+) ; pKMS6

<220>

<221> misc\_feature

<222> (190)..(225)

<223> primer

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<222> (190)..(207)

<223> cys tag

<220>

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<222> (936)..(956)

<223> primer

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Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
20 25 30

Gly Ser Cys Cys Cys Cys Cys Cys Ser Leu Gln Asp Glu Ala Leu Lys  
35 40 45

Ala Trp Gln Ala Arg Tyr Gly Glu Pro Ala Asn Leu Pro Ala Ala Asp  
50 55 60

Thr Val Ile Ala Gln Met Leu Gln His Arg Ser Val Arg Ala Tyr Ser  
65 70 75 80

Asp Leu Pro Val Asp Glu Gln Met Leu Ser Trp Ala Ile Ala Ala Ala  
85 90 95

Gln Ser Ala Ser Thr Ser Ser Asn Leu Gln Ala Trp Ser Val Leu Ala  
100 105 110

Val Arg Asp Arg Glu Arg Leu Ala Arg Leu Ala Arg Leu Ser Gly Asn  
115 120 125

Gln Arg His Val Glu Gln Ala Pro Leu Phe Leu Val Trp Leu Val Asp  
130 135 140

Trp Ser Arg Leu Arg Arg Leu Ala Arg Thr Leu Gln Ala Pro Thr Ala  
145 150 155 160

Gly Ile Asp Tyr Leu Glu Ser Tyr Thr Val Gly Val Val Asp Ala Ala  
165 170 175

Leu Ala Ala Gln Asn Ala Ala Leu Ala Phe Glu Ala Gln Gly Leu Gly  
180 185 190

Ile Val Tyr Ile Gly Gly Met Arg Asn His Pro Glu Ala Met Ser Glu



195

200

205

Glu Leu Gly Leu Pro Asn Asp Thr Phe Ala Val Phe Gly Met Cys Val  
210 215 220

Gly His Pro Asp Pro Ala Gln Pro Ala Glu Ile Lys Pro Arg Leu Ala  
225 230 235 240

Gln Ser Val Val Leu His Arg Glu Arg Tyr Glu Ala Thr Glu Ala Glu  
245 250 255

Ala Val Ser Val Ala Ala Tyr Asp Arg Arg Met Ser Asp Phe Gln His  
260 265 270

Arg Gln Gln Arg Glu Asn Arg Ser Trp Ser Ser Gln Ala Val Glu Arg  
275 280 285

Val Lys Gly Ala Asp Ser Leu Ser Gly Arg His Arg Leu Arg Asp Ala